

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M. Ruben

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SmithKline Beecham Corporation
- (B) STREET: 709 Swedeland Road
- (C) CITY: King of Prussia
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/018,961
- (B) FILING DATE: 05 JUNE 1996

- (A) APPLICATION NUMBER: 60/020,344
- (B) FILING DATE: 23 MAY 1996

- (A) APPLICATION NUMBER: 60/017,949
- (B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Han, William T.
- (B) REGISTRATION NUMBER: 34,344
- (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5219
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Glu	Ala	Asp	Arg	Arg	Leu	Leu	Arg	Arg	Cys	Arg	Leu	Arg	Leu
1					5				10					15	
Val	Glu	Glu	Leu	Gln	Val	Asp	Gln	Leu	Trp	Asp	Val	Leu	Leu	Ser	Arg
					20				25					30	
Glu	Leu	Phe	Arg	Pro	His	Met	Ile	Glu	Asp	Ile	Gln	Arg	Ala	Gly	Ser
					35			40						45	
Gly	Ser	Arg	Arg	Asp	Gln	Ala	Arg	Gln	Leu	Ile	Ile	Asp	Leu	Glu	Thr
					50			55						60	
Arg	Gly	Ser	Gln	Ala	Leu	Pro	Leu	Phe	Ile	Ser	Cys	Leu	Glu	Asp	Thr
					65			70			75			80	
Gly	Gln	Asp	Met	Leu	Ala	Ser	Phe	Leu	Arg	Thr	Asn	Arg	Gln	Ala	Gly
					85			90						95	
Lys	Leu	Ser	Lys	Pro	Thr	Leu	Glu	Asn	Leu	Thr	Pro	Val	Val	Leu	Arg
					100			105						110	
Pro	Glu	Ile	Arg	Lys	Pro	Glu	Val	Leu	Arg	Pro	Glu	Thr	Pro	Arg	Pro
					115			120						125	
Val	Asp	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser
					130			135						140	

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG	AAGCGGATCG	CGGGCTCCTG	CGGCGGTGCC	GGCTGCGGCT	GGTGGAAAGAG	60
CTGCAGGTGG	ACCAGCTCTG	GGACGCTCCTG	CTGAGCCGCG	AGCTGTTCA	GCCCCATATG	120
ATCGAGGACA	TCCAGCGGGC	AGGCTCTGGA	TCTCGGCGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGAGG	GAGTCAGGCT	CTTCCTTTGT	TCATCTCCTG	CTTAGAGGAC	240
ACAGGCCAGG	ACATGCTGGC	TTCGTTTCTG	CGAACTAAC	GGCAAGCAGG	AAAGTTGTCG	300
AAGCCAACCC	TAGAAAACCT	TACCCCAGTG	GTGCTCAGAC	CAGAGATTG	CAAACCAGAG	360
GTTCTCAGAC	CGGAAACACC	CAGACCAGTG	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGCCTTTG	AGAGTTGAG	GGGAAATGCA	GATTTGGCTT	ACATCCTGAG	CATGGAGCCC	480
TGTGGCCACT	GCCTCATTAT	CAACAAATGTG	AACTTCTGCC	GTGAGTCCGG	GCTCCGCACC	540
CGCACTGGCT	CCAACATCGA	CTGTGAGAAG	TTGCGGCGTC	GCTTCTCCTC	GCTGCATTTC	600
ATGGTGGAGG	TGAAGGGCGA	CCTGACTGCC	AAGAAAATGG	TGCTGGCTTT	GCTGGAGCTG	660
GCGCGGCAGG	ACCACGGTGC	TCTGGACTGC	TGCGTGGTGG	TCATTCTCTC	TCACGGCTGT	720
CAGGCCAGCC	ACCTGCAGTT	CCCACGGGCT	GTCTACGGCA	CAGATGGATG	CCCTGTGTCG	780
GTCGAGAAGA	TTGTGAACAT	CTTCAATGGG	ACCAGCTGCC	CCAGCCTGGG	AGGGAAAGCCC	840
AAGCTCTTTT	TCATCCAGGC	CTGTGGTGGG	GAGCAGAAAG	ACCATGGGTT	TGAGGTGGCC	900
TCCACTTCCC	CTGAAGACGA	GTCCCCCTGGC	AGTAACCCCC	AGCCAGATGC	CACCCCGTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACCCAGCTG	GACGCCATAT	CTAGTTGCC	CACACCCAGT	1020
GACATCTTTG	TGTCCCTACTC	TACTTTCCCA	GGTTTTGTTT	CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCCTGGT	ACGTTGAGAC	CCTGGACGAC	ATCTTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGCAGTC	TCCTGCTTAG	GGTCGCTAAT	GCTGTTTCCG	TGAAAGGGAT	TTATAAACAG	1200
ATGCCTGGTT	GCTTTAATTT	CCTCCGGAAA	AAACTTTTCT	TTAAAACATC	ATAAGGCCAG	1260
GGCCCCCTCAC	CCTGCCTTAT	CTTGCACCCCC	AAAGCTTTCC	TGCCCCCAGGC	CTGAAAGAGG	1320
CTGAGGCCTG	GACTTTCCG	CAACTCAAGG	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTT	1380
CTCTGCCAGT	GACAGACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTGG	NCTCTTGAGC	AGTGGCTGGT	1500
CCAGGGCTAG	TGACTTGGTG	TCCCAGATC	CCTGTGTTGG	TCTCTAGGAG	CAGGGATTAA	1560
CCTCTGCACT	ACTGACAT					1578

- (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GCGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTGTCGG	TCGAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCC	CAGCCTGGGA	GGGAAGCCCA	AGCTCTTTT	CATCCAGGCC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCCT	CCACTTCCCC	TGAAGACGAG	300
TCCCCCTGGCA	GTAACCCCGA	GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG	ACGCCATATC	TAGTTGCC	ACACCCAGTG	ACATCTTGT	GTCCTACTCT	420
ACTTTCCCAG	GTTTTGTTTC	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTC	600
CTCCGGAAAA	AACTTTTCTT	TTAAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu				
1	5	10	15	
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His				
	20	25	30	
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser				
	35	40	45	
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu				
	50	55	60	
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln				

65	70	75	80
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser			
85	90	95	
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu			
100	105	110	
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser			
115	120	125	
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg			
130	135	140	
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe			
145	150	155	160
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Arg Val			
165	170	175	
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys			
180	185	190	
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met			
195	200		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAACGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCA^T CGTCGTC^CTT GTAGTCTGAT GTTTAAAGT TAAGTTTTT

60

CCGGAG

66

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KIKLY, KRISTINE K.
RUBEN, STEVEN M.

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING
ENZYME LIKE APOPTOTIC PROTEASE-6

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/952,936
(B) FILING DATE: 08-MAY-1997
(C) CLASSIFICATION: UNKNOWN

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/013,961
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p30483-2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
1 5 10 15
Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
20 25 30
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
35 40 45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
50 55 60
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
65 70 75 80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
85 90 95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
100 105 110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
115 120 125
Val Asp Ile Gly Ser Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
130 135 140
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
145 150 155 160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
165 170 175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
180 185 190
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
195 200 205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
210 215 220
Gly Ala Leu Asp Cys Cys Val Val Ile Leu Ser His Gly Cys Gln
225 230 235 240
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
245 250 255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
260 265 270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
275 280 285
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
290 295 300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
305 310 315 320
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
325 330 335
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
340 345 350
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
355 360 365

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu			
370	375	380	
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met			
385	390	395	400
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser			
405	410	415	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG	60
CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCGCG AGCTGTTCTG GCCCCATATG	120
ATCGAGGACA TCCAGGGGGC AGGCTCTGGG TCTCGGGGGG ATCAGGCCAG GCAGCTGATC	180
ATAGATCTGG AGACTCGAGG GAGTCAGGCT TTTCCTTGTG TCACTCTCTG CTTAGAGGAC	240
ACAGGCCAGG ACATGCTGGC TTCTGTTCTG CGAACTAACAGGAAAGTTGTCG	300
AAGCCAACCC TAGAAAACCT TACCCAGTG GTGCTCAGAC CAGAGATTCTG CAAACCAGAG	360
GTTCTCAGAC CGGAAACACC CAGACCAAGTG GACATTGGTT CTGGAGGATT CGGTGATGTC	420
GGTGCCTTGAG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC	480
TGTGGCCACT GCCTCATTAT CAACATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC	540
CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCAGGCTG GCTCTCTC GCTGCATTTC	600
ATGGTGGAGG TGAAGGGCGA CCTGACTGCG AAGAAAATGG TGCTGGCTTT GCTGGAGCTG	660
GCCCGGCAGG ACCACGGTGC TCTGGACTGC TGCAGGGTGG TCATTCTCTC TCACGGCTGT	720
CAGGCCAGCC ACCTGGCAGTT CCCAGGGCT GTCTACGGCA CAGATGGATG CCGCTGTGTCG	780
GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAAGCCC	840
AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGCC	900
TCCACTTCCC CTGAAGACGA GTCCCTGCG AGTAAACCCCG AGCCAGATGC CACCCCGTTC	960
CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT	1020
GAGATCTTTG TGTCTACTC TACTTTCCCA GGTGTTGTTT CCTGGAGGGG CCCCAGAGT	1080
GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC	1140
CTGCAGTCCC TCTGCTTAG GGTGCGTAT GCTGTTTGG TGAAAGGGAT TTATAAACAG	1200
ATGCCCTGGTT GCTTTAATT CTCGGGAAA AAACTTTCT TTAAAACATC ATAAGGCCAG	1260
GGCCCCCTAC CCTGCCTTAT CTGGCACCCCC AAAGCTTCCG TGCCCCAGGC CTGAAAGAGG	1320
CTGAGGCCCTG GACTTTCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTT	1380
CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAAACAGT	1440
GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT	1500
CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTGG TCTCTAGGAG CAGGGATTA	1560
CCTCTGCACT ACTGACAT	1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GGCTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTGTCGG	TCGAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCC	CAGCCTGGGA	GGGAAGCCCCA	AGCTCTTTT	CATCCAGGCC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCCT	CCACTCCCC	TGAAGACGAG	300
TCCCCTGGCA	GTAAACCCGA	GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG	ACGCCATATC	TAGTTGCCC	ACACCCAGTG	ACATCTTGT	GTCCTACTCT	420
ACTTTCCAG	GTTTGTTTC	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTC	600
CTCCGGAAAA	AACTTTCTT	TTAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Leu	Ala	Leu	Glu	Leu	Ala	Arg	Gln	Asp	His	Gly	Ala	Leu	
1								10					15		
Asp	Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His
			20				25						30		
Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	Pro	Val	Ser
			35				40						45		
Val	Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	Pro	Val	Ser
			50				55						60		
Gly	Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Gly	Gly	Glu	Gln
			65				70						75		80
Lys	Asp	Asp	Gly	Phe	Glu	Val	Ala	Ser	Thr	Ser	Pro	Glu	Asp	Glu	Ser
			85				90						95		
Pro	Gly	Ser	Asn	Pro	Glu	Pro	Asp	Ala	Thr	Pro	Phe	Gln	Glu	Gly	Leu
			100				105						110		
Arg	Thr	Phe	Asp	Gln	Leu	Asp	Ala	Ile	Ser	Ser	Leu	Pro	Thr	Pro	Ser
			115				120						125		
Asp	Ile	Phe	Val	Ser	Tyr	Ser	Thr	Phe	Pro	Gly	Phe	Val	Ser	Trp	Arg
			130				135						140		
Asp	Pro	Lys	Ser	Gly	Ser	Trp	Tyr	Val	Glu	Thr	Leu	Asp	Asp	Ile	Phe
			145				150						155		160
Glu	Gln	Trp	Ala	His	Ser	Glu	Asp	Leu	Gln	Ser	Leu	Leu	Leu	Arg	Val
			165				170						175		
Ala	Asn	Ala	Val	Ser	Val	Lys	Gly	Ile	Tyr	Lys	Gln	Met	Pro	Gly	Cys
			180				185						190		
Phe	Asn	Phe	Leu	Arg	Lys	Lys	Leu	Phe	Phe	Met					
			195				200								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CGGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT AAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTGAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTT 60
CCGGAG 66

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Gly Gly
1 5